

maryh@stic

3148-1

NeWSprinter20

Tue Jul 01 14:59:27 1997 ✓

NeWSprint 2.5 Rev B

Openwin library 3

NeWSprint interpreter 210.0

NeWSprint 2.5

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MAQSEARCH

(TM)

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Release 2.1D John F. Collins, Biocomputing Research Unit.  
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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Jul 1 13:06:26 1997; MacPar time 45.21 Seconds  
255.216 Million cell updates/sec

Tabular output not generated.

Title: >US-08-726-211-1  
Description: (1-18) from US08726211.1.aeq  
Perfect Score: 18  
N.A. Sequence: 1 CAGCGTGGCCATCCTTC 18  
Comp: GTCGACCGGTAGGAAG

Scoring table: TABLE default  
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 887282 seqs, 320523884 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database:

EST-STS  
1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8  
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14  
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20  
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26  
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32  
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38  
39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44  
45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST50  
51:EST51 52:EST52 53:EST53 54:EST54 55:EST55 56:EST56  
57:EST57 58:EST58 59:EST59 60:EST60 61:EST61 62:EST62  
63:EST63 64:EST64 65:EST65 66:EST66 67:EST67 68:EST68  
69:EST69 70:EST70 71:EST71 72:EST72 73:EST73 74:EST74  
75:EST75 76:EST76 77:EST77 78:EST78 79:EST79 80:EST80  
81:EST81 82:EST82 83:EST83 84:EST84 85:EST85 86:EST86  
87:EST87 88:EST88 89:EST89 90:EST90 91:EST91 92:EST92  
93:EST93 94:EST94 95:EST95 96:EST96 97:EST97 98:EST98  
99:EST99  
EST-STS-TWO  
100:EST100 101:EST101 102:EST102 103:EST103 104:EST104  
105:EST105 106:EST106 107:EST107 108:EST108 109:EST109

Database:

Statistics: Mean 6.072; Variance 1.188; scale 5.113

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	IDB	ID	Description	Pred. No.
c	1	14	77.8	266	93	MD57JF05	Mouse embryonal carci	4.26e-02
c	2	14	77.8	300	65	HSC2QF011	H. sapiens partial cD	4.26e-02
c	3	14	77.8	448	52	H79390	yu48e02.r1 Homo sapie	4.26e-02
c	4	14	77.8	453	175	W66944	me29d08.r1 Soares mou	4.26e-02
5	14	77.8	563	211	N95054	zb32c05.e1 Homo sapie	4.26e-02	
6	14	77.8	563	118	N95054	zb32c05.e1 Homo sapie	4.26e-02	
7	14	77.8	638	12	AA005111	zh96g10.r1 Soares fet	4.26e-02	
c	8	13	72.2	92	122	R86574	RABEST145M Oryctolagu	8.03e-01
9	13	72.2	241	218	T93415	ImEST0178 LMLV39CDNA	8.03e-01	
10	13	72.2	241	151	T93415	ImEST0178 LMLV39CDNA	8.03e-01	
11	13	72.2	257	151	T93466	ImEST0236 LMLV39CDNA	8.03e-01	
12	13	72.2	265	151	T93448	ImEST0218 LMLV39CDNA	8.03e-01	
13	13	72.2	265	218	T93448	ImEST0218 LMLV39CDNA	8.03e-01	
14	13	72.2	301	64	HSC26F041	H. sapiens partial cD	8.03e-01	
c	15	13	72.2	316	47	CEK127B1R	C.elegans cDNA clone	8.03e-01
c	16	13	72.2	328	243	MAA52315	mb15e05.r1 Soares mou	8.03e-01
c	17	13	72.2	328	10	AA052315	mb15e05.r1 Soares mou	8.03e-01

110:EST110 111:EST111 112:EST112 113:EST113 114:EST114  
115:EST115 116:EST116 117:EST117 118:EST118 119:EST119  
120:EST120 121:EST121 122:EST122 123:EST123 124:EST124  
125:EST125 126:EST126 127:EST127 128:EST128 129:EST129  
130:EST130 131:EST131 132:EST132 133:EST133 134:EST134  
135:EST135 136:EST136 137:EST137 138:EST138 139:EST139  
140:EST140 141:EST141 142:EST142 143:EST143 144:EST144  
145:EST145 146:EST146 147:EST147 148:EST148 149:EST149  
150:EST150 151:EST151 152:EST152 153:EST153 154:EST154  
155:EST155 156:EST156 157:EST157 158:EST158 159:EST159  
160:EST160 161:EST161 162:EST162 163:EST163 164:EST164  
165:EST165 166:EST166 167:EST167 168:EST168 169:EST169  
170:EST170 171:EST171 172:EST172 173:EST173 174:EST174  
175:EST175 176:EST176 177:EST177 178:EST178 179:EST179  
180:EST180 181:EST181 182:EST182 183:EST183 184:EST184  
185:EST185 186:EST186 187:EST187 188:EST188 189:EST189  
190:EST190 191:EST191 192:EST192 193:EST193

Database:

EST-STS-THREE

194:STS1 195:STS2 196:STS3 197:STS4 198:STS5 199:STS6  
200:STS7 201:STS8 202:STS9 203:STS10 204:STS11 205:STS12  
206:STS13 207:STS14 208:STS15 209:STS16 210:STS17  
211:STS18 212:STS19 213:STS20 214:STS21 215:STS22  
216:STS23 217:STS24 218:STS25 219:STS26  
220:STS27 221:STS28 222:STS29 223:STS30 224:STS31  
225:STS32 226:STS33 227:STS34 228:STS35 229:STS36  
230:STS37 231:STS38 232:STS39 233:STS40 234:STS41  
235:STS42 236:STS43 237:STS44 238:STS45  
239:STS46 240:STS47 241:STS48 242:STS49  
243:STS50 244:STS51 245:STS52 246:STS53  
247:STS54 248:STS55 249:STS56 250:STS57  
251:STS58

c 18 13 72.2 330 44 CELK011D1F C.elegans cDNA clone 8.05e-01  
c 19 13 72.2 345 54 H85998 yw13c09.r1 Homo sapie 8.05e-01  
c 20 13 72.2 350 241 MNA30151 mi25g06.r1 Soares mou 8.05e-01  
c 21 13 72.2 354 160 T47853 yb17f04.r1 Homo sapie 8.05e-01  
c 22 13 72.2 371 123 R89144 yp99f08.r1 Homo sapie 8.05e-01  
c 23 13 72.2 396 181 W84983 mfa3b09.r1 Soares mou 8.05e-01  
c 24 13 72.2 399 248 MNA86816 mm85h10.r1 Soares mou 8.05e-01  
c 25 13 72.2 402 244 MNA66262 mm41g11.r1 Stratagene 8.05e-01  
c 26 13 72.2 402 151 AA066262 y05e08.r1 Homo sapie 8.05e-01  
c 27 13 72.2 405 151 T93841 y137b11.r1 Homo sapie 8.05e-01  
c 28 13 72.2 412 138 R68970 Human fetal brain cDN 8.05e-01  
c 29 13 72.2 419 89 HDW133C09B y136g04.r1 Homo sapie 8.05e-01  
c 30 13 72.2 434 136 R64449 za35a12.r1 Soares fet 8.05e-01  
c 31 13 72.2 444 155 W03227 za35a12.r1 Soares fet 8.05e-01  
c 32 13 72.2 444 213 W03227 43 vegetative meriste 8.05e-01  
c 33 13 72.2 450 250 ZM6491 43 Zea mays cDNA clon 8.05e-01  
c 34 13 72.2 450 145 T70649 TgESTzy56g12.r1 TGRHc 8.05e-01  
c 35 13 72.2 468 250 TGA37940 mj45b06.r1 Soares mou 8.05e-01  
c 36 13 72.2 469 9 AA048837 TgESTzy09g12.r1 Toxop 8.05e-01  
c 37 13 72.2 495 87 N60488 TgESTzy09g12.r1 Toxop 8.05e-01  
c 38 13 72.2 495 207 N60488 zk29a03.r1 Soares pre 8.05e-01  
c 39 13 72.2 498 228 HSA36796 yz30d03.r1 Homo sapie 8.05e-01  
c 40 13 72.2 515 113 N76173 yz30d03.r1 Homo sapie 8.05e-01  
c 41 13 72.2 515 208 N76173 mk17f01.r1 Soares mou 8.05e-01  
c 42 13 72.2 541 249 MNA97487 zn46c11.r1 Stratagene 8.05e-01  
c 43 13 72.2 569 234 HSA4446 mb50b11.r1 Soares mou 8.05e-01  
c 44 13 72.2 1049 215 W08459 mb50b11.r1 Soares mou 8.05e-01  
c 45 13 72.2 1049 163 W08459

## ALIGNMENTS

1 MUS77F05 266 bp mRNA EST 04-OCT-1996  
LOCUS Mouse embryonal carcinoma F9 cell cDNA, 77F05.  
DEFINITION D76820  
ACCESSION g1596548  
NID EST (expressed sequence tag).  
KEYWORDS Mus musculus  
SOURCE Mus musculus cell\_line:F9 cell cDNA to mRNA.  
ORGANISM Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 266)  
AUTHORS Shimada,K.  
TITLE Direct Submission  
JOURNAL Submitted (26-SEP-1995) to the DDBJ/EMBL/GenBank databases.  
Kazunori Shimada, Research Institute for Microbial Diseases, Osaka University, Department of Medical Genetics; 3-1 Yamadaoka, Suita, Osaka 565, Japan (E-mail:f61246@center.osaka-u.ac.jp, Tel:06-879-8325, Fax:06-879-8326)  
REFERENCE 2 (bases 1 to 266)  
AUTHORS Nishiguchi,S., Sakuma,R., Nomura,M., Zou,Z., Jearanaisilavong,J., Joh,T., Yasunaga,T. and Shimada,K.  
TITLE A catalogue of genes in mouse embryonal carcinoma F9 cells  
J. Blochem 119, 749-767 (1996)  
J. Blochem 119, 749-767 (1996)  
LOCATION/Qualifiers 1..266  
FEATURES  
source /organism="Mus musculus"

BASE COUNT 69 a 71 c 76 g 47 t 3 others  
ORIGIN  
Query Match 77.8%; Score 14; DB 93; Length 266;  
Best Local Similarity 93.8%; Pred. No. 4.26e-02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 185 aggatggcgccacctg 200  
|||||  
Cp 16 AGCATGGCGCAGCTG 1  
|||||  
RESULT 2 HSC2Q2011 300 bp RNA EST 21-SEP-1995  
LOCUS H. sapiens partial cDNA sequence; clone c-2q01.  
DEFINITION Z49480  
ACCESSION g574694  
NID partial cDNA sequence; transcribed sequence fragment.  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 300)  
AUTHORS Genexpress.  
TITLE Direct Submission  
JOURNAL Submitted (24-OCT-1994) Genethon, B.P. 60, 91002 Evry Cedex France and Genetique Moleculaire et Biologie du developpement, CNRS UPR420 B.P. 8, 94801 Villejuif Cedex France.E-mail: genexpress@genethon.fr  
REFERENCE 2 (bases 1 to 300)  
AUTHORS Genexpress.  
TITLE The Genexpress cDNA program  
JOURNAL Unpublished  
AUTHORS 3 (bases 1 to 300)  
Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houllatte,R., Jumeau,M.N., Lamv,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y., Sebastiani-Kabatchia,C. and Terasier,A.  
IMAGE: molecular integration of the analysis of the human genome and its expression  
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)  
95277534  
COMMENT Clone library from B.Souares, Psychiatry Dept. Columbia University USA;  
Cloning\_method: total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA vector;  
Sequencing method: single read, full automatic;  
Primer: M13 reverse  
cDNA sequence colinear to mRNA  
Stretch removed: nothing  
Normalization method: Bento Soares, P.N.A.S in press;  
Genexpress library idt: C;  
Genexpress\_sequence\_idt: y1c-2q01;  
No significant homology found with :  
genbank release 83 swissprot release 28.  
LOCATION/Qualifiers 1..300  
FEATURES  
source

```

/organism="Homo sapiens"
/isolate="muscular atrophy patient"
/dev_stage="3 months old"
/tissue_type="total brain"
/clone_lib="normalized infant brain cDNA"
/sex="Female"
77 q 83 q 62 t

```

BASE COUNT	78 a	77 c	83 g	62 t
ORIGIN				
Query Match		77.8%	Score 14;	DB 65; Length 300;
Best Local Similarity		88.9%;	Pred. No. 4.26e-02;	
Matches	16;	Conservative	0;	Mismatches 2; Indels 0; Caps 0;

Query Match 77.8%; Score 14; DB 65; Length 300;  
Best Local Similarity 88.9%; Pred. No. 4.26e-02;

Db 218 gaaggattgcgaccctg 235  
||||| ||||| |||||  
Cp 18 GAAGGATGCCGCACGCTG 1

RESULT	3				
LOCUS	H79390	448 bp	mRNA	EST	
DEFINITION	U44802.r1 Homo sapiens cDNA clone 229370 5'.				
ACCESSION	H79390				
	NID	g1057479			
KEYWORDS	EST.				

Es: human clone-229370 primer-M13RPI library-Soares fetal liver spleen  
 nFLTS vector=PT73D (Pharmacia) with a modified polylinker  
 host=DH10B (ampicillin resistant) Reitel=Pac I Raite2=Eco RI Liver  
 and spleen from a 20 week-post conception male fetus. 1st strand  
 cDNA was primed with a Pac I - oligo(dT) primer [5'  
 ACTGCGAGATTAATTAAGACATCTTTTCTTTTCTTTT 3'], double-stranded  
 cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac  
 I and cloned into the Pac I and Eco RI sites of the modified pT73  
 vector. Library went through one round of normalization. Library  
 constructed by Bento Soares and M.Fatima Bonaldo.

## ORGANISM

Homio sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

## REFERENCE AUTHORS

1 (bases 1 to 448)  
 Hillier, L., Clark, N., Dubuque, T., Ellistat, K., Hawkins, M.,  
 Holman, M., Lullman, M., Kucaba, T., Le M., Lennon, G., Marra, M.,  
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
 Trevasik, E., Waterston, R., Williamson, A., Wohlmann, P. and  
 Wilson, R.

**TITLE**  
**JOURNAL**  
**WILSON, K.**  
**The WashU-Merck EST Project**  
**Unpublished (1995)**

**JOURNAL  
COMMENT**

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

FAX: 314 200 1000  
 Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)  
 High quality sequence stops: 332

This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
 Location/Qualifiers

## FEATURES

Location/Qualification

```

source      1..448
            /organism="Homo sapiens"
            /clone="229370"
            <1..5448
mRNA
BASE COUNT 118 a   93 c  111 g  124 t
ORIGIN      2 others

```

Query Match 77.8%; Score 14; DB 52; Length 448;  
Best Local Similarity 88.9%; Pred. No. 4.26e-02;  
Matches 16; Conservative 0; Mismatches 2; Indels

58 aaagaaattacacaccca 75

Cp 18 GAAGGATGGCGCAGCTG 1

## RESULT 4

LOCUS	W65944	453 bp	mRNA	EST	14-JUN-1996
DEFINITION	me29d08.r1 Soares mouse embryo NBME13.5 14.5 Mus musculus cDNA clone 388911 5' similar to PIR:S44218 S44218 testin - mouse [1] ;				
ACCESSION	W65944				
NID	g1375887				
KEYWORDS	EST.				

NETWORKS	EST.	house mouse.
SOURCE		
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Source: *House mouse*.  
 ORGANISM: *Mus musculus*  
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 453)

**AUTHORS**  
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geiser, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schnellberg, K., Stepcoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

**TITLE**

JOURNAL  
UNPUBLISHED (1996)COUNT  
COMMENT

Contact: Marra M/Mouse EST Project  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8301, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LINL ; con-  
IMAGE Consortium (info@image.linl.gov) for further info  
MGI:240743

High quality sequence stop: 348.

Location/Qualifiers

source

```

/organism="Mus musculus"
/strain="C57BL/6J"
/notes="Vector: pr73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo (dT) primer [5',
TGTACCACTCTGAAGTGGAGCGCGCGAATTTTTTTTTTTTTT
T], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 l; double-stranded cDNA was ligated to

```

Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

/clone.lib="Soares mouse embryo NbME13.5 14.5"  
/seq="unknown"  
/tissue\_type="embryo"  
/dev\_stage="13.5-14.5dpc total fetus"  
/lab\_host="DH10B"  
<1..>453

BASE COUNT 111 a 120 c 140 g 82 t  
ORIGIN

Query Match 77.8%; Score 14; DB 175; Length 453;  
Best Local Similarity 88.9%; Pred. No. 4.26e-02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 333 gaagatgtgcacctg 350  
|||||  
Cp 18 GAAGATGGCGCAGCTG 1

RESULT 5 N95054 563 bp mRNA EST 09-APR-1996  
LOCUS Zb32c05.s1 Homo sapiens cDNA clone 305288 3' similar to PIR:S44218  
DEFINITION S44218 testin - mouse [1] ;  
ACCESSION N95054  
NID g1267343

KEYWORDS EST.  
SOURCE human clone=305288 primer=ETPrimer library=Soares parathyroid tumor  
NbHPA vector=pT713D (Pharmacia) with a modified polylinker  
host=DH10B (ampicillin resistant) Reitel=Not I Raite2=Eco RI Adult.  
1st strand cDNA was primed with a Not I - oligo(dT) primer  
[5'-TGTTACCAATCTGAAGTGGCGCGCAGCAATTTTTTTTTTTTTTTTTTTT-  
3'], double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of a modified pT713 vector (Pharmacia). Library  
went through one round of normalization to a Cot = 5. Library  
constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic  
parathyroid adenomas was kindly provided by Dr. Stephen Marx,  
National Institute of Diabetes and Digestive and Kidney Diseases,  
NIH.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 563)  
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marrá,M.,  
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
Trevaakie,E., Waterston,R., Williamson,A., Wohlmann,P. and  
Wilson,R.

TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK  
WashU-Merck EST Project

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

High quality sequence stops: 84  
Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

Possible reversed clone: polyf not found.

NCBI gi: 1267343  
FEATURES  
source  
Location/Qualifiers  
1..563  
/organism="Homo sapiens"  
/clone="305288"  
/note="human"  
<1..>563

BASE COUNT 103 a 159 c 162 g 130 t 9 others  
ORIGIN

Query Match 77.8%; Score 14; DB 211; Length 563;  
Best Local Similarity 88.9%; Pred. No. 4.26e-02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 11 cagggtgcacctctc 28  
|||||  
Cp 1 CAGCGTGGCCATCCTC 18

RESULT 6 N95054 563 bp mRNA EST 09-APR-1996  
LOCUS Zb32c05.s1 Homo sapiens cDNA clone 305288 3' similar to PIR:S44218  
DEFINITION S44218 testin - mouse [1] ;  
ACCESSION N95054  
NID g1267343

KEYWORDS EST.  
SOURCE human clone=305288 primer=ETPrimer library=Soares parathyroid tumor  
NbHPA vector=pT713D (Pharmacia) with a modified polylinker  
host=DH10B (ampicillin resistant) Reitel=Not I Raite2=Eco RI Adult.  
1st strand cDNA was primed with a Not I - oligo(dT) primer  
[5'-TGTTACCAATCTGAAGTGGCGCGCAGCAATTTTTTTTTTTTTTTTTTTT-  
3'], double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of a modified pT713 vector (Pharmacia). Library  
went through one round of normalization to a Cot = 5. Library  
constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic  
parathyroid adenomas was kindly provided by Dr. Stephen Marx,  
National Institute of Diabetes and Digestive and Kidney Diseases,  
NIH.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 563)  
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marrá,M.,  
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
Trevaakie,E., Waterston,R., Williamson,A., Wohlmann,P. and  
Wilson,R.



JOURNAL Bone 17 (2), 111-119 (1995)  
MEDLINE 96021365  
COMMENT Other ESTs: RABEST149T  
Contact: Sakai D  
Basic Sciences  
University of Southern California  
USC School of Dentistry, 925 West 34th Street, DEN-4220, Los  
Angeles, CA 90089-0641  
Tel: 2137403563  
Fax: 2137407560  
Email: sakai@molbio.usc.edu.  
FEATURES Location/Qualifiers  
source 1..92  
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/strain="New Zealand White"  
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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DEFINITION IMEST0178 LmLV39cDNA Leishmania major cDNA clone Im244 5' END.  
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NID 9726588  
KEYWORDS EST.  
SOURCE Leishmania major.  
ORGANISM Leishmania major  
Eukaryotes; mitochondrial eukaryotes; Euglenozoa; Kinetoplastida;  
Trypanosomatidae; Leishmania.  
REFERENCE 1 (bases 1 to 241)  
AUTHORS Ajioaka, J.W.  
TITLE Leishmania major cDNAs  
JOURNAL Unpublished (1995)  
COMMENT Contact: Ajioaka JW  
Laboratory for Parasite Genome Analysis  
Cambridge University  
Department of Pathology, Tennis Court Road, Cambridge CB2 1QP, UK.  
Tel: 01223333923  
Fax: 01223333923  
Email: jajioaka@hmp.mrc.ac.uk  
Seq primer: T3.  
NCBI gi: 726588  
FEATURES Location/Qualifiers  
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/strain="LV39"  
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Mid or late log promastigotes.Full\_length : splice leader

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ACCESSION T93415  
NID 9726588  
KEYWORDS EST.  
SOURCE Leishmania major.  
ORGANISM Leishmania major  
Eukaryotes; mitochondrial eukaryotes; Euglenozoa; Kinetoplastida;  
Trypanosomatidae; Leishmania.  
REFERENCE 1 (bases 1 to 241)  
AUTHORS Ajioaka, J.W.  
TITLE Leishmania major cDNAs  
JOURNAL Unpublished (1995)  
COMMENT Contact: Ajioaka JW  
Laboratory for Parasite Genome Analysis  
Cambridge University  
Department of Pathology, Tennis Court Road, Cambridge CB2 1QP, UK.  
Tel: 01223333923  
Fax: 01223333923  
Email: jajioaka@hmp.mrc.ac.uk  
Seq primer: T3.  
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cloning NotI at 5' end, XhoI at 3' end."  
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 6 TCGGCATCCTTC 18

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LOCUS T93466 257 bp mRNA EST 01-MAY-1996  
DEFINITION lmeST0236 LmLV39cDNA Leishmania major cDNA clone lme43 5' END.  
ACCESSION T93466  
NID 9726639  
KEYWORDS EST.  
SOURCE Leishmania major.  
ORGANISM Leishmania major  
Eukaryotes; mitochondrial eukaryotes; Euglenozoa; Kinetoplastida;  
Trypanosomatidae; Leishmania.

REFERENCE  
AUTHORS Ajioka, J.W.  
TITLE Leishmania major cDNAs  
JOURNAL Unpublished (1995)  
COMMENT Contact: Ajioka JW  
Laboratory for Parasite Genome Analysis  
Cambridge University  
Department of Pathology, Tennis Court Road, Cambridge CB2 1QP, UK.  
Tel: 01223333923  
Fax: 01223333923  
Email: jajioka@hmp.mrc.ac.uk  
Seq primer: T3.

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cloning NotI at 5' end, XhoI at 3' end."  
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ACCESSION T93448  
NID 9726621  
KEYWORDS EST.  
SOURCE Leishmania major.  
ORGANISM Leishmania major  
Eukaryotes; mitochondrial eukaryotes; Euglenozoa; Kinetoplastida;

Trypanosomatidae; Leishmania.

REFERENCE  
AUTHORS Ajioka, J.W.  
TITLE Leishmania major cDNAs  
JOURNAL Unpublished (1995)  
COMMENT Contact: Ajioka JW  
Laboratory for Parasite Genome Analysis  
Cambridge University  
Department of Pathology, Tennis Court Road, Cambridge CB2 1QP, UK.  
Tel: 01223333923  
Fax: 01223333923  
Email: jajioka@hmp.mrc.ac.uk  
Seq primer: T3.

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cloning NotI at 5' end, XhoI at 3' end."  
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QY 6 TCGGCATCCTTC 18

RESULT 13  
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DEFINITION lmeST0218 LmLV39cDNA Leishmania major cDNA clone lme390 5' END.  
ACCESSION T93448  
NID 9726621  
KEYWORDS EST.  
SOURCE Leishmania major.  
ORGANISM Leishmania major  
Eukaryotes; mitochondrial eukaryotes; Euglenozoa; Kinetoplastida;  
Trypanosomatidae; Leishmania.

REFERENCE  
AUTHORS Ajioka, J.W.  
TITLE Leishmania major cDNAs  
JOURNAL Unpublished (1995)  
COMMENT Contact: Ajioka JW  
Laboratory for Parasite Genome Analysis  
Cambridge University  
Department of Pathology, Tennis Court Road, Cambridge CB2 1QP, UK.  
Tel: 01223333923  
Fax: 01223333923  
Email: jajioka@hmp.mrc.ac.uk



Seq primer: T3.

NCBI gi: 726621  
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oligo used for second strand synthesis, directional  
cloning NotI at 5' end, XhoI at 3' end."  
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Qy 6 TGGCCATCCTTC 18

RESULT 14  
LOCUS HSC26F041 301 bp RNA EST 21-SEP-1995  
DEFINITION H. sapiens partial cDNA sequence; clone c-26F04.  
ACCESSION F07460  
NID 9673120  
KEYWORDS partial cDNA sequence; transcribed sequence fragment.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Genexpress.  
Direct Submission  
Submitted (19-JAN-1995) Genethon, B.P. 60, 91002 Evry Cedex France  
and Genetique Moleculaire et Biologie du developpement, CNRS UPR420  
B.P. 8, 94801 Villejuif Cedex France E-mail: genexpress@genethon.fr  
2 (bases 1 to 301)  
Genexpress.  
The Genexpress cDNA program  
Unpublished  
3 (bases 1 to 301)  
Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C.,  
Designes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B.,  
Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y.,  
Sebastiani-Kabaktchis, C. and Tessier, A.  
IMAGE: molecular integration of the analysis of the human genome  
and its expression  
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)  
95277334

JOURNAL  
MEDLINE  
COMMENT  
Cloning method: total mRNA was oligo-(dT) primed and directionally  
cloned 5' -> 3' into the HindIII -> NotI sites of the lfaIId BA  
vector;  
Sequencing\_method: single read, full automatic;

Primer: M13 reverse  
cDNA sequence colinear to mRNA  
Stretch\_removed: nothing  
Normalization\_method: Bento Soares, P.N.A.S. 91:9228-9232(1994);  
Genexpress\_library\_id: C;  
Genexpress\_sequence\_id: Y1C-26F04.  
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Psychiatry Dept. Columbia University USA"  
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RESULT 15  
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DEFINITION C.elegans cDNA clone yk127b1 : 3' end, single read.  
ACCESSION D64881  
NID Q1117323  
KEYWORDS EST(expressed sequence tag).  
SOURCE Yuji Kohara unpublished cDNA) Hermaphrodite, male varied whole  
animal cDNA to mRNA.  
ORGANISM Caenorhabditis elegans  
Eukaryotes; mitochondrial eukaryotes; Metazoa; Nematoda;  
Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;  
Rhabditidae; Caenorhabditis.  
Kohara, Y., Motoshashi, T., Tabara, H., Sugimoto, A., Watanabe, H. and  
Nishigaki, A.  
1 (bases 1 to 316)  
Toward an expression map of the C.elegans genome  
Unpublished (1995)  
Submitted (23-Aug-1995) to DDBJ by:  
Yuji Kohara  
Gene Library Lab.  
National Institute of Genetics  
Yata 1111, Mishima Shizuoka  
411 Japan  
Phone: 0559-81-6854  
Fax : 0559-81-6855  
Email: ykoha@dbj.nig.ac.jp.  
Location/Qualifiers  
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Matches 14; Conservative 0; Mismatches 1; Indels

Search completed: Tue Jul 1 13:14:41 1997  
Job time : 495 secs.

maryh@stic

3149-1

NeWSprinter20

Tue Jul 01 15:00:23 1997

NeWSprint 2.5 Rev B

Openwin library 3

NeWSprint interpreter 210.0

NeWSprint 2.5

\*\*\*\*\*

MAJESTY (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.  
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Distribution rights by Intelligent, Inc.

MParch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Jul 1 12:58:46 1997; MacPar time 37.84 Seconds  
Tabular output not generated. 528.936 Million cell updates/sec

Title: >US-08-726-211-1  
Description: (1-18) from US08726211.1.seq  
Perfect Score: 18  
N.A. Sequence: 1 CAGCGTGGCCATGCTTC 18  
Comp: GTCCGACGCGGTAGGAAG

Scoring table:

Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 333249 seqs, 555961234 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

emb1-new11  
1:BCT 2:FUN 3:GEN 4:HOM1 5:HOM2 6:HOM3 7:INV1 8:INV2  
9:INV3 10:INV4 11:INV5 12:INV6 13:INV7 14:ORG 15:MAM  
16:VRT 17:PLN 18:PRO1 19:PRO2 20:ROD 21:SYN 22:UNC  
23:VIR1 24:VIR2

Database:

genbank97  
25:BCT1 26:BCT2 27:BCT3 28:BCT4 29:BCT5 30:BCT6 31:BCT7  
32:BCT8 33:BCT9 34:GEN1 35:GEN2 36:HTG 37:INV1 38:INV2  
39:INV3 40:INV4 41:INV5 42:INV6 43:INV7 44:INV8 45:INV9  
46:MAM1 47:MAM2 48:MAM3 49:VRT1 50:VRT2 51:VRT3 52:PAT1  
53:PAT2 54:PAT3 55:PAT4 56:PHG 57:PLN1 58:PLN2 59:PLN3  
60:PLN4 61:PLN5 62:PLN6 63:PLN7 64:PLN8 65:PLN9 66:PLN10  
67:PLN11 68:PLN12 69:PLN13 70:PLN14 71:PLN15 72:PLN16 73:PLN17  
74:PLN18 75:PLN19 76:PLN20 77:PLN21 78:PLN22 79:PLN23  
80:PLN24 81:ROD1 82:ROD2 83:ROD3 84:ROD4 85:ROD5 86:ROD6  
87:ROD7 88:ROD8 89:STR 90:SYN 91:UNA 92:VRL1 93:VRL2  
94:VRL3 95:VRL4 96:VRL5 97:VRL6 98:VRL7 99:VRL8 100:VRL9

Database:

genbank-new11  
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113:UNA 114:VRL

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115:part1 116:part2

Statistics: Mean 6.349; Variance 2.406; scale 2.639

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	3	18	100.0	5086	75	HUMBCL2A	Human B-cell leukemia	5.71e-02	
c	4	18	100.0	5105	54	I08038	Sequence 1 from Paten	5.71e-02	
c	5	16	88.9	1708	31	RMNODD2X	Rhizobium tropical nod	1.85e+00	
c	6	16	88.9	1846	70	HSBCL2IG	H.sapiens mRNA for bc	1.85e+00	
c	7	15	83.3	1083	101	BHU52149	Borrelia hermsii vari	9.73e+00	
c	8	15	83.3	1083	18	BHU52149	Borrelia hermsii vari	9.73e+00	
c	9	14	77.8	29	49	CHKC2A101	Chicken alpha-1 type-	4.79e+01	
c	10	14	77.8	364	48	S46866	PEC-60-gaastrointestin	4.79e+01	
c	11	14	77.8	364	48	SPECC60	S.scrofa PEC-60 mRNA.	4.79e+01	
c	12	14	77.8	450	48	SFBPRNA	S.scrofa mRNA for pla	4.79e+01	
c	13	14	77.8	700	80	S72412	proteoglycan versican	4.79e+01	
c	14	14	77.8	1179	86	RATBCL2A	Rattus norvegicus bcl	4.79e+01	
c	15	14	77.8	1429	53	A19155	ovine IL-1 beta.	4.79e+01	
c	16	14	77.8	1930	50	GGCETS2	Chicken mRNA for c-et	4.79e+01	
c	17	14	77.8	2087	109	HUMPGH3A	Human pgh3 mRNA for p	4.79e+01	
c	18	14	77.8	2087	78	HUMPGH3A	Human pgh3 mRNA for p	4.79e+01	
c	19	14	77.8	2135	80	SS2488	CSPG2-vascular core	4.79e+01	
c	20	14	77.8	2340	27	ECOTOPB	E.coli topoisomerase	4.79e+01	
c	21	14	77.8	2914	84	MUSBCL21	Mouse bcl-2 gene enco	4.79e+01	
c	22	14	77.8	3204	30	NGO60099	Neisseria gonorrhoeae	4.79e+01	
c	23	14	77.8	5923	74	HSU26555	Human versican V2 cor	4.79e+01	
c	24	14	77.8	5932	41	DROC4A1A	D.melanogaster collag	4.79e+01	
c	25	14	77.8	5946	41	DROC4A1A	D.melanogaster collag	4.79e+01	
c	26	14	77.8	6030	75	HUMBCL2C	Human bcl-2 mRNA.	4.79e+01	
c	27	14	77.8	7972	40	DDRN05	Dictyostelium discoid	4.79e+01	
c	28	14	77.8	8224	75	HSVERS	H.sapiens mRNA for th	4.79e+01	
c	29	14	77.8	8541	41	DROC4L4G	Drosophila melanogast	4.79e+01	
c	30	14	77.8	11185	73	HSU16306	Human chondroitin sul	4.79e+01	
c	31	14	77.8	12733	25	ATUORF	Agrobacterium rhizoge	4.79e+01	
c	32	14	77.8	28888	38	CELC41G11	Caenorhabditis elegan	4.79e+01	
c	33	14	77.8	28888	8	CELC41G11	Caenorhabditis elegan	4.79e+01	
c	34	13	72.2	2425	84	MUSERMBP	Mouse ecotropic retro	2.20e+02	
c	35	13	72.2	3529	30	MTU60588	Mycobacterium tubercu	2.20e+02	
c	36	13	72.2	4993	19	PP04052	Pseudomonas pickettii	2.20e+02	
c	37	13	72.2	5437	31	PSEFUS	P.sepacia fusaric aci	2.20e+02	
c	38	13	72.2	6591	20	MIPAE7	Podospora anserina m	2.20e+02	
c	39	13	72.2	6492	67	ECODMS	E.coli dmsA, dmsB and	2.20e+02	
c	40	13	72.2	6892	65	SPUR11	S.pombe mRNA for URA1	2.20e+02	
c	41	13	72.2	7391	26	BORVMPGG	Borrelia hermsii rear	2.20e+02	
c	42	13	72.2	23349	12	CEZC306	Caenorhabditis elegan	2.20e+02	
c	43	13	72.2	23349	39	CEZC306	Caenorhabditis elegan	2.20e+02	
c	44	13	72.2	36241	30	ML015186	Mycobacterium leprae	2.20e+02	
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 ACCESSION S72602  
 NID g241046  
 KEYWORDS human 697 pre-B cell acute lymphocytic leukemia cell line.  
 SOURCE Homo sapiens  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 454)  
 AUTHORS Tanaka, S., Louie, D.C., Kant, J.A. and Reed, J.C.  
 TITLE Frequent incidence of somatic mutations in translocated BCL2  
 oncogenes of non-Hodgkin's lymphomas  
 JOURNAL Blood 79 (1), 229-237 (1992)  
 MEDLINE 92096610  
 REMARK GenBank staff at the National Library of Medicine created this  
 entry [NCBI gibbsq 72602] from the original journal article.  
 This sequence comes from Fig.2.

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 BASE COUNT 65 a 170 c 150 g 69 t  
 ORIGIN

Query Match 100.0%; Score 18; DB 80; Length 454;  
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 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 36 gaagatggcgcacgtg 53  
 Cp 18 GAAGATGGCGCAGCTG 1

2 HUMBCL2B 911 bp mRNA PRI 31-OCT-1994  
 LOCUS Human B-cell leukemia/lymphoma 2 (bcl-2) proto-oncogene mRNA  
 DEFINITION encoding bcl-2-beta protein, complete cds.  
 ACCESSION M13995  
 NID g179368  
 KEYWORDS alternative splicing; bcl-2-beta protein; proto-oncogene.  
 SOURCE Human pre-B-cell leukemia cell line 380, cDNA to mRNA, clones  
 B15,161; and DNA, clone lambda-18-27.

ORGANISM Homo sapiens  
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 911)  
 AUTHORS Tanjinoto, Y. and Croce, C.M.  
 TITLE Analysis of the structure, transcripts, and protein products of  
 bcl-2, the gene involved in human follicular lymphoma

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 83 (14), 5214-5218 (1986)  
 MEDLINE 86259760  
 COMMENT Clean copy sequence for [1] kindly provided by Y.Taujimoto,  
 10-FEB-1987. The bcl-2 gene is transcribed by alternative splicing  
 into three mRNAs of different sizes. It consists of at least two  
 exons and encodes two proteins which only differ at their  
 carboxy-terminal ends, and it is activated by translocation into  
 proximity with the Ig heavy chain locus. Both the normal and  
 rearranged bcl-2 gene products are expressed in the B-cell  
 leukemia/lymphoma 2 cells. Genomic clone lambda-18-27 contained  
 all the DNA sequences on the 5' of the splice site (position 732).

FEATURES  
 source 1..911  
 location/Qualifiers  
 /organism="Homo sapiens"  
 /map="18q21.3"  
 mRNA <1..>911  
 CDS 147..764

/gene="BCL2"  
 /note="bcl2-beta protein"  
 /codon\_start=1  
 /db\_xref="GDB:G00-119-031"  
 /db\_xref="PID:g179369"  
 /translation="MAHAGRTGYDNRINVKYIHYKLSQRYEWADGVGAAPGAAP  
 APGIFSQGHTPHPAASRDVPARTSPLOTAPAAAGAAAGPALSPPVPPVHLALRQAGD  
 DFSRRYRGDFAEMSSQLHLTFPTARGRFA"  
 misc\_feature SVNREMSPLVDNIALMTYINRHLHTWIDNGWVGASGVSLG"  
 732  
 /gene="BCL2"  
 /note="alternative splice donor (intron A start)"  
 BASE COUNT 156 a 281 c 306 g 168 t  
 ORIGIN 556 bp upstream of SstI site.

Query Match 100.0%; Score 18; DB 73; Length 911;  
 Best Local Similarity 100.0%; Pred. No. 5.71e-02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 142 gaagatggcgcacgtg 159  
 Cp 18 GAAGATGGCGCAGCTG 1

3 HUMBCL2A 5086 bp mRNA PRI 31-OCT-1994  
 LOCUS Human B-cell leukemia/lymphoma 2 (bcl-2) proto-oncogene mRNA  
 DEFINITION encoding bcl-2-alpha protein, complete cds.  
 ACCESSION M13994  
 NID g179366  
 KEYWORDS alternative splicing; bcl-2-alpha protein; proto-oncogene.  
 SOURCE Human pre-B-cell leukemia cell line 380, cDNA to mRNA, clones  
 B13,4,101; and DNA, clone lambda-18-27.

ORGANISM Homo sapiens  
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 5086)  
 AUTHORS Tanjinoto, Y. and Croce, C.M.  
 TITLE Analysis of the structure, transcripts, and protein products of  
 bcl-2, the gene involved in human follicular lymphoma  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 83 (14), 5214-5218 (1986)  
 MEDLINE 86259760

## COMMENT

Clean copy sequence for [1] kindly provided by Y.Tsujimoto, 10-FEB-1987.  
The bcl-2 gene is transcribed by alternative splicing into three mRNAs of different sizes. It consists of at least two exons and encodes two proteins which only differ at their carboxy-terminal ends, and it is activated by translocation into proximity with the Ig heavy chain locus. Both the normal and rearranged bcl-2 gene products are expressed in the B-cell leukemia/lymphoma 2 cells. Genomic clone lambda-18-27 contained all the DNA sequences on the 3' of the splice site (position 2044).

## FEATURES

source

Location/Qualifiers

1..5086

/organism="Homo sapiens"

/map="18q21.3"

1..5086

/note="bcl2a mRNA"

1459..2178

/gene="BCL2"

/note="bcl2-alpha protein"

/codon\_start=1

/db\_xref="GDB:G00-119-031"

/db\_xref="PID:g179367"

/translation="MAHAGRTGVDNREIVNKYIHYKLSQGYEWDAAGVGAAPGCAAP  
APGIFSSQGHTPHAPASRDVPARTSLQTPAAPGAAGPALSPPVHVHLARQAGD  
DFSRRYRGDFAEMSSQLHLTPFTARGFATVVEELFDGVNMGRIVARFEFGVMQVE  
SYNREMSPLVDNIATWTEYLNRHLHTWIDQNGWDAFVELYGPSMRPLDFEWSLSLK  
TLLSALVGACITIGAYLSHK"

BASE COUNT 1262 a 1224 c 1287 g 1313 t

ORIGIN 710 bp upstream of Set1 site.

Query Match 100.0%; Score 18; DB 75; Length 5086;  
Best Local Similarity 100.0%; Pred. No. 5.71e-02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1454 gaagatggcgcacgtg 1471

|||||

Cp 18 GAAGATGGCGCAGCTG 1

## RESULT 4

LOCUS

I08038

PAT

14-NOV-1994

DEFINITION Sequence 1 from Patent EP 0252685.

ACCESSION I08038

NID 9589249

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 5105)

AUTHORS Tsujimoto,Y. and Croce,C.M.

TITLE Diagnostic methods for detecting lymphomas in humans

JOURNAL Patent: EP 0252685-A2 1 13-JAN-1986;

## FEATURES

source

Location/Qualifiers

1..5105

/organism="unknown"

BASE COUNT 1281 a 1224 c 1287 g 1313 t

ORIGIN

Query Match 100.0%; Score 18; DB 54; Length 5105;

Best Local Similarity 100.0%; Pred. No. 5.71e-02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1454 gaagatggcgcacgtg 1471

|||||

Cp 18 GAAGATGGCGCAGCTG 1

## RESULT 5

LOCUS

RHMODD2X

1708 bp

DNA

BCT

09-MAR-1993

DEFINITION

Rhizobium tropici nodulation protein D (nodD2) gene, complete cds.

ACCESSION

L01272

NID 9152365

KEYWORDS

nodD gene; nodulation protein D; regulatory protein.

SOURCE

Rhizobium tropici (strain BR816) DNA.

ORGANISM

Eubacteria; Proteobacteria; alpha subdivision; Rhizobiaceae;

Rhizobium.

REFERENCE 1 (bases 1 to 1708)

AUTHORS van Rhijn,P.J.S., Feys,B. and Vanderleyden,J.

TITLE Multiple copies of nodD in Rhizobium tropici CIAT899 and BR816

JOURNAL J. Bacteriol. 175, 438-447 (1993)

MEDLINE

93123162

FEATURES

Location/Qualifiers

1..1708

/organism="Rhizobium tropici"

/strain="BR816"

435..1379

/gene="nodD2"

/note="putative"

/codon\_start=1

/function="regulatory protein"

/product="nodulation protein D"

/db\_xref="PID:g152366"

/transl\_table=11

/translation="MRFGDLNLVLDALMTERNLTAARSINLSQPSAAVARL  
RTNFRDDLAMAGREFTPTPRAEGLAPVADLLOLSIVSWEPNPAQSDRRFRIV  
LSDYVTLVFEKVVAAQAEAGISFDCLPLADDFELLRRGDIDFLMPELFSMHP  
HAALFEDKVCVCGRTNEQSEFTFTFERMSMGHVAKFNTNRPTIEWYLLHGLK  
RRIEVVVQGFSTMPPLMSGTGRTPLRLAQHFAKFTPLRIVELPLPIPLAEAVQW  
PALHNSDPASILMWRELLQLQASLMVSPRAPVRLSAPGF"

misc\_binding

495..538

/gene="nodD2"

/note="putative"

/function="transcription regulation"

/bound\_moiety="helix-turn-helix DNA-binding"

BASE COUNT 325 a 472 c 488 g 423 t

ORIGIN

Query Match 88.9%; Score 16; DB 31; Length 1708;  
Best Local Similarity 94.4%; Pred. No. 1.85e+00;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1612 cagctggcgcacatcttc 1629

|||||

Qy 1 CAGCTGGCCCATCCTTC 18

## RESULT 6

LOCUS

HSBCL2IG

1846 bp

RNA

PRI

26-MAR-1993



G  
FT E RSLSEVLMEVCKSAENAFYSFMALVSDTLGLRVTKDKKNEVCGYFNSLGGKGLKASD  
FT E LEEVAKKSEVEGAKDGPITAVAIRAADVDTAKTTTLTKLGHLESILKIGDDKVVGVWAEND  
Q QGIRKPADDLGNLFNALQSIVKAAATDAGVLAPKAGNTTLTVNGVDNKGOKAVLAIDKP  
G AAVEGKASLIIVSAVSGEELIASIVASKEGQALGAADGTTTAMSAKGGTKDNLNSA  
FT N TPKAAVAGGIALRSLVKDGLASHNDNSEKAVQAAGVIAANKLLVSVEDLIKKTVKN  
FT V LEKAKEIKDKARAPKATQQ"  
SQ Sequence 1083 BP; 440 A; 137 C; 270 G; 236 T; 0 other;  
Query Match 83.3%; Score 15; DB 18; Length 1083;  
Best Local Similarity 100.0%; Pred. No. 9.73e+00;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 105 gaagatggcgacg 119  
|||||  
Cp 18 GAAGGATGGCGCAGC 4

RESULT 9  
LOCUS CHKC2A101 29 bp DNA VRT 23-MAY-1996  
DEFINITION Chicken alpha-1 type-II collagen gene; amino acids 578 to 585.  
ACCESSION K02260  
NID 9211336  
KEYWORDS alpha-1 type II collagen; collagen.  
SEGMENT 1 of 6  
SOURCE Gallus gallus (clone: LgCOL(II)). DNA.  
ORGANISM Gallus gallus  
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Archosauria; Aves; Neognathae; Galliformes;  
Phasianidae; Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 29)  
AUTHORS Sandell, L.J., Yamada, Y., Dorfman, A. and Upholt, W.B.  
TITLE Identification of genomic DNA coding for chicken type II procollagen  
J. Biol. Chem. 258 (19), 11617-11621 (1983)  
MEDLINE 84008159  
COMMENT Each procollagen gene codes for the six successive functional regions of the protein: signal peptide, NH-2 propeptide, NH-2 telopeptide, helical peptide, COOH telopeptide, and COOH propeptide. The type-II COOH-propeptide is cleaved from the procollagen molecule after the triple helical molecule is secreted into the extracellular matrix.  
FEATURES  
source 1..29  
/organism="Gallus gallus"  
/clone="LgCOL(II)."  
/cell type="reticulocyte"  
<1..24  
/note="preprocollagen alpha-1 type-II, AA 578 to 585"  
/codon start=1  
25..>29  
Intron  
/note="collagen intron"  
BASE COUNT 7 a 7 c 11 g 4 t  
ORIGIN Downstream of EcoRI site.

Query Match 77.8%; Score 14; DB 49; Length 29;  
Best Local Similarity 100.0%; Pred. No. 4.79e+01;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 10 aagatggcgacg 23  
|||||  
Cp 17 AAGGATGGCGCAGC 4

RESULT 10  
LOCUS S46866 364 bp mRNA MAM 05-JAN-1993  
DEFINITION PEC-60-gastrointestinal peptide (swine, duodenum, mRNA, 364 nt).  
ACCESSION S46866  
NID 9257597  
KEYWORDS swine duodenum.  
SOURCE Sus sp.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 364)  
AUTHORS Meteis, M., Cintra, A., Solfrini, V., Ernfor, P., Bortolotti, F., Morrasutti, D.G., Ostenson, C.G., Efendic, S., Agerberth, B., Mutt, V. et, al.  
TITLE Molecular cloning of PEC-60 and expression of its mRNA and peptide in the gastrointestinal tract and immune system  
J. Biol. Chem. 267 (28), 19829-19832 (1992)  
MEDLINE 93015834  
REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibseq 115614] from the original journal article.  
This sequence comes from Fig. 1.  
FEATURES  
source 1..364  
/organism="Sus sp."  
/db\_xref="PID:g257598"  
/note="gastrointestinal peptide; Author includes translated amino acids 5' of putative initiation codon; This sequence comes from Fig. 1. Author-given protein sequence is in conflict with the conceptual translation"  
/codon\_start=1  
/product="PEC-60"  
/db\_xref="PID:g257598"  
/translation="RRQPRISMARVRLMWVALAALFIVDREVPVSAEKQVFSRNPIC EHMTESPDCSRIVDPVCGTGVTESECKLCLARIENKQDIOIVKDGEC"  
BASE COUNT 91 a 93 c 108 g 72 t  
ORIGIN

Query Match 77.8%; Score 14; DB 48; Length 364;  
Best Local Similarity 88.9%; Pred. No. 4.79e+01;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Db 265 gaagatggcgacg 282  
|||||  
Cp 18 GAAGGATGGCGCAGC 1

RESULT 11  
LOCUS SSPEC60 364 bp RNA MAM 06-JUL-1992  
DEFINITION S.acrofa PEC-60 mRNA.  
ACCESSION X67109  
NID g2033  
KEYWORDS pec-60 gene.



SOURCE pig.  
ORGANISM Sus scrofa  
REFERENCE Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
1 (bases 1 to 364) Vertebrata; Eutheria; Artiodactyla; Suiformes; Suina; Suidae; Sus.  
AUTHORS Metais.M.  
TITLE Direct Submission  
JOURNAL Submitted (22-JUN-1992) M. Metais, Dept. of Medical Chemistry, Lab.  
of Molecular Neurobiology, Karolinska Institute, Box 604 00, 10401  
Stockholm, SWEDEN

FEATURES Location/Qualifiers  
source 1..364  
/organism="Sus scrofa"  
/clone\_lib="pig duodenal cDNA library in gt10 4x10 6"  
CDS 23..283  
/evidence=experimental  
/codon\_start=1  
/product="peptide PEC-60"  
/db\_xref="PID:g2034"  
/translation="MAVFLWVALAALFVIREVPSAEKQVFSRMPICHTWTEPS  
DCSRIYDPCGTDGVTYESECKLARIENKQDIQIVKGE"  
23..76  
/note="peptide PEC-60"  
mat\_peptide 101..280  
/product="peptide PEC-60"  
BASE COUNT 91 a 93 c 108 g 72 t  
ORIGIN  
Query Match 77.8%; Score 14; DB 48; Length 364;  
Best Local Similarity 88.9%; Pred. No. 4.79e+01;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Db 265 gaagtgatggcgatgctg 282  
|||||  
Cp 18 GAAGGATGGCGGACGCTG 1

RESULT 12  
LOCUS SSPBRNA 450 bp RNA MAM 06-JUL-1994  
DEFINITION S.scrofa mRNA for platelet basic protein.  
ACCESSION X77935  
NID 9457753  
KEYWORDS platelet basic protein.  
SOURCE pig.  
ORGANISM Sus scrofa  
REFERENCE Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
1 (bases 1 to 450) Vertebrata; Eutheria; Artiodactyla; Suiformes; Suina; Suidae; Sus.  
AUTHORS Power,C.A., Proudfoot,A.E., Magnenat,E., Bacon,K.B. and Wells,T.N.  
TITLE Molecular cloning and characterisation of a neutrophil chemotactic  
protein from porcine platelets  
JOURNAL Eur. J. Biochem. 221 (2), 713-719 (1994)  
MEDLINE 94229068  
REFERENCE 2 (bases 1 to 450)  
AUTHORS Power,C.A.  
TITLE Direct Submission  
JOURNAL Submitted (01-MAR-1994) C.A. Power, Glaxo Institute for Molecular  
Biology, 14 chemin des Auxix, 1228 Plan-les-Ouates, Geneva,  
SWITZERLAND

FEATURES Location/Qualifiers  
source 1..450  
/organism="Sus scrofa"  
/clone\_lib="lambda zapII porcine platelet cDNA library"  
1..450  
/gene="CTAPIII/NAP-2"  
/product="platelet basic protein"  
CDS 91..450  
/gene="CTAPIII/NAP-2"  
/codon\_start=1  
/product="platelet basic protein"  
/db\_xref="PID:g457754"  
/translation="MSLRGAISSCTTSSPFPVLQVLLSLTLVTPATGCAAKIE  
GRMAHVEIRCLINTVSGIHPSNIQSLVIRAGAHCAKVEVIAITLKNDRKICLDPEAP  
RIKKIVQKIMEDGGSA"  
190..447  
mat\_peptide 110 a 128 c 109 g 103 t  
/gene="CTAPIII/NAP-2"  
/product="platelet basic protein"  
BASE COUNT 110 a 128 c 109 g 103 t  
ORIGIN  
Query Match 77.8%; Score 14; DB 48; Length 450;  
Best Local Similarity 88.9%; Pred. No. 4.79e+01;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Db 224 gaagaatggcgacgttg 241  
|||||  
Cp 18 GAAGGATGGCGGACGCTG 1

RESULT 13  
LOCUS S72412 700 bp mRNA PRI 28-APR-1995  
DEFINITION proteoglycan versican=large chondroitin sulfate proteoglycan  
{PCR-1} [monkeys, smooth muscle cells, juvenile aorta, mRNA  
Partial, 700 nt].  
ACCESSION S72412  
NID 9786543  
KEYWORDS monkeys juvenile aorta smooth muscle cells.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 700)  
AUTHORS Yao,L.Y., Moody,C., Schonherr,E., Wight,T.N. and Sandell,L.J.  
TITLE Identification of the proteoglycan versican in aorta and smooth  
muscle cells by DNA sequence analysis, in situ hybridization and  
immunohistochemistry  
JOURNAL Matrix Biol. 14 (3), 213-225 (1994)  
MEDLINE 95005762  
REMARK GenBank staff at the National Library of Medicine created this  
entry (NCBI gisbaq 152611) from the original journal article.  
This sequence comes from Fig. 5.

FEATURES Location/Qualifiers  
source 1..700  
/organism="unknown"  
/note="monkeys"  
1..699  
/partial  
/note="Description: proteoglycan versican, CSPG; large  
chondroitin sulfate proteoglycan; mismatch(50[V->A]); This

sequence comes from Fig. 5. Author-given protein sequence is in conflict with the conceptual translation"

/codon\_start=1  
/product="proteoglycan veraican"  
/db\_xref="PID:g786544"  
/translation="YPIRAPVGCYGMGKAGVRYTGFSPQETVDVYCYVDHLDGD  
VFHLTVPSKFTFEAAKECENQARLATVGELOAAWNGFDQDYGWLSDAVSRHPVT  
VARCGGGLLGVRTLYRFENQGTGPPDPDFDAYCFKRMSSDLVIGHPIDSEKED  
EPCSETDPVHDLMAEILPEFPDIIIDLYHSENEEEECANADVTITFSQVIN  
GKHLYTVPKPEAA"

BASE COUNT 191 a 155 c 192 g 162 t  
ORIGIN

Query Match 77.8%; Score 14; DB 80; Length 700;  
Best Local Similarity 93.8%; Pred. No. 4.79e+01;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 285 cagcgtgcccaccct 300  
|||||  
QY 1 CAGCGTGGCCATCCT 16

RESULT 14  
LOCUS RATBCL2A 1179 bp mRNA ROD 28-NOV-1994  
DEFINITION Rattus norvegicus bcl-2 mRNA, complete cds.  
ACCESSION L14680  
NID g408946  
KEYWORDS bcl-2 gene; dinucleotide repeat; oncogene.  
SOURCE Rattus norvegicus (library: Clontech; TS95-11-2) brain cDNA to mRNA.

ORGANISM Rattus norvegicus  
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;  
Murinae; Rattus.

REFERENCE 1 (bases 1 to 1179)  
AUTHORS Sato, I., Irie, S., Krajewski, S. and Reed, J.C.  
TITLE Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein  
JOURNAL Gene 140 (2), 291-292 (1994)  
MEDLINE 94193015

FEATURES Location/Qualifiers  
source 1..1179  
/organism="Rattus norvegicus"  
/tissue type="brain"  
/tissue lib="Clontech; TS95-11-2"  
CDS 235..945  
/gene="bcl-2"  
/codon\_start=1

/db\_xref="PID:g408947"  
/translation="MAQAGRTGYDREIVMKYIHYKLSQRYEWDTGDEDSAPLRAAP  
TPGIFSFOESNRTPAVHRDTAARTSPRLVANAGPALSPPVPPVHLTLRAGDDFS  
RMYRRDFAEMSSQLHPTFTARGRTAVTVELFRDGVNWRGIVAFEFEGVMCVGSYN  
REMSPLVDNIALMWTVELNRLHHTWIQDNGWDFAVELYGPSMRPLDFDSWLSIKTL  
SLALVGATILGAYLGHK"

repeat\_region 1061..1112  
polya\_site /rpt unit=1061..1062  
BASE COUNT 295 a 316 c 306 g 262 t  
ORIGIN

Query Match 77.8%; Score 14; DB 86; Length 1179;

Best Local Similarity 93.8%; Pred. No. 4.79e+01;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 230 gaaggatggcgcaagc 245  
|||||  
Cp 18 GAAGGATGGCGCAGC 3

RESULT 15  
LOCUS A19155 1429 bp RNA PAT 09-MAY-1994  
DEFINITION ovine IL-1 beta.  
ACCESSION A19155  
NID g512009  
KEYWORDS Ovis sp..  
SOURCE Ovis sp..  
ORGANISM Ovis sp..  
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Artiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Caprinae; Ovis.  
REFERENCE 1 (bases 1 to 1429)

AUTHORS  
TITLE CYTOKINE PRODUCTION  
JOURNAL Patent: WO 9203574-A 18 05-MAR-1992;

FEATURES Location/Qualifiers  
source 1..1429  
/organism="Ovis sp."  
CDS 46..846  
/codon\_start=1  
/product="ovine IL-1 beta"  
/db\_xref="PID:g512010"

/translation="MATVPEINEMVAYSDENELLFEVDGPKQKSCQHLDLGSMG  
DGNQLQISHOLYNKSFQVSVIVAMEKLSRAYEHVFRDDLRSLIFPEEPVI  
FETSSDELLCDAAVQSVKCKLQDREOKSLVSPCKALHLLSOEMSEVVFQMSFV  
QGEERDNKIPVALGIRDKNLYLSCVKGDTPTLQLEEDVPKVPYPRNMEKRFVFKTE  
IKNTVEFESLYPNWYISTSQIEKFPVLGRFRGGDITDFRMETLSP"  
BASE COUNT 416 a 363 c 315 g 335 t  
ORIGIN

Query Match 77.8%; Score 14; DB 53; Length 1429;  
Best Local Similarity 100.0%; Pred. No. 4.79e+01;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1284 gtgcgcacatccttc 1297  
|||||  
QY 5 GTGCGCCATCCTTC 18

Search completed: Tue Jul 1 13:05:12 1997  
Job time : 386 secs.

maryh@stic

3147-1

NeWSprinter20

Tue Jul 01 14:58:39 1997

NeWSprint 2.5 Rev B

Openwin library 3

NeWSprint interpreter 210.0

NeWSprint 2.5

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 MAY 1994  
 \*\*\*\*\* (TM)  
 \*\*\*\*\*

Release 2.1D John F. Collins, Biocomputing Research Unit.  
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MParch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Jul 1 13:05:29 1997; MasPar time 5.23 Seconds  
 Tabular output not generated. 318.173 Million cell updates/sec

Title: >US-08-726-211-1  
 Description: (1-18) from US08726211.seq  
 Perfect Score: 18  
 N.A. Sequence: 1 CAGCGTGGCCATCTTC 18  
 Comp: GTCCACGCGTAGGAAG

Scoring table: TABLE default  
 Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 121476 seqs, 46255616 bases x 2

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: n-geneseq26  
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
 14:part14 15:part15 16:part16 17:part17 18:part18  
 19:part19 20:part20 21:part21 22:part22 23:part23

Statistics: Mean 4.967; Variance 2.625; scale 1.892

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
c 1	18	100.0	20	14	Q86649 Bcl-2 translation ini	3.98e-02
2	18	100.0	22	8	Q49817 Bcl-2 antisense oligo	3.98e-02
3	18	100.0	22	8	Q49816 Bcl-2 antisense oligo	3.98e-02
c 4	18	100.0	35	14	Q86644 Bcl-2 translation ini	3.98e-02

c	5	18	100.0	765	8	Q49815	Bcl-2.	3.98e-02
c	6	18	100.0	831	1	N81293	Sequence of bcl-2 cDN	3.98e-02
c	7	18	100.0	5086	14	Q86661	Human bcl-2 gene.	3.98e-02
c	8	18	100.0	5086	9	Q54631	Human oncogene bcl-2	3.98e-02
c	9	18	100.0	5105	1	N81292	Sequence of bcl-2 cDN	3.98e-02
c	10	17	94.4	91	9	Q51746	Oligonucleotide probe	1.66e-01
c	11	16	88.9	91	9	Q51746	Oligonucleotide probe	6.76e-01
c	12	14	77.8	1429	3	Q22825	Sequence encoding ovi	1.02e+01
c	13	14	77.8	1359	10	Q56983	Improved Heat-stable	1.02e+01
c	14	14	77.8	1359	10	Q56981	Improved Heat-stable	1.02e+01
c	15	14	77.8	1359	10	Q56989	Heat-stable carbamyla	1.02e+01
c	16	14	77.8	1359	10	Q56979	Improved Heat-stable	1.02e+01
c	17	14	77.8	1359	10	Q56991	Heat-stable carbamyla	1.02e+01
c	18	14	77.8	1359	10	Q56984	Improved Heat-stable	1.02e+01
c	19	14	77.8	1359	10	Q56980	Improved Heat-stable	1.02e+01
c	20	14	77.8	1359	10	Q56982	Improved Heat-stable	1.02e+01
c	21	14	77.8	1784	10	Q56976	Heat-stable carbamyla	1.02e+01
c	22	14	77.8	1785	10	Q56971	Heat-stable carbamyla	1.02e+01
c	23	14	77.8	1785	10	Q56963	Heat-stable carbamyla	1.02e+01
c	24	14	77.8	1785	10	Q56967	Heat-stable carbamyla	1.02e+01
c	25	14	77.8	1785	10	Q56990	Heat-stable carbamyla	1.02e+01
c	26	14	77.8	1785	10	Q56966	Heat-stable carbamyla	1.02e+01
c	27	14	77.8	1785	10	Q56968	Heat-stable carbamyla	1.02e+01
c	28	14	77.8	1785	10	Q56974	Heat-stable carbamyla	1.02e+01
c	29	14	77.8	1785	10	Q56964	Heat-stable carbamyla	1.02e+01
c	30	14	77.8	1785	10	Q56993	Heat-stable carbamyla	1.02e+01
c	31	14	77.8	1785	10	Q56987	Heat-stable carbamyla	1.02e+01
c	32	14	77.8	1785	4	Q26090	KNK-712.	1.02e+01
c	33	14	77.8	1785	10	Q56986	Heat-stable carbamyla	1.02e+01
c	34	14	77.8	1785	10	Q56970	Heat-stable carbamyla	1.02e+01
c	35	14	77.8	1785	10	Q56994	Heat-stable carbamyla	1.02e+01
c	36	14	77.8	1785	10	Q56969	Heat-stable carbamyla	1.02e+01
c	37	14	77.8	1785	10	Q56978	Heat-stable carbamyla	1.02e+01
c	38	14	77.8	1785	10	Q56972	Heat-stable carbamyla	1.02e+01
c	39	14	77.8	1785	10	Q56992	Heat-stable carbamyla	1.02e+01
c	40	14	77.8	1785	10	Q56977	Heat-stable carbamyla	1.02e+01
c	41	14	77.8	1785	10	Q56975	Heat-stable carbamyla	1.02e+01
c	42	14	77.8	1785	10	Q56988	Heat-stable carbamyla	1.02e+01
c	43	14	77.8	1785	10	Q56973	Heat-stable carbamyla	1.02e+01
c	44	14	77.8	1785	10	Q56965	Heat-stable carbamyla	1.02e+01
c	45	14	77.8	8224	2	Q12261	Versican gene.	1.02e+01

ALIGNMENTS

RESULT 1  
 ID Q86649 standard; DNA; 20 BP.  
 AC Q86649;  
 DT 27-SEP-1995 (first entry)  
 DE Bcl-2 translation initiation site region.  
 KW Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;  
 KW lymphoma; programmed cell death; as.  
 OS Synthetic.  
 PN WO9508350-A.  
 PD 30-MAR-1995.  
 PF 20-SEP-1994; U10725.  
 PR 20-SEP-1993; US-124256.  
 PA (REED/) REED J C.  
 PI Reed JC;  
 DR WPI; 95-139394/18.

PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment  
PT of human solid tumours, esp. breast cancer  
PS Example 12; Page 33; 108pp; English.  
CC Antisense oligonucleotides were tested for their ability to induce  
CC programmed cell death (DNA fragmentation) in the human lymphoma cell  
CC line RS11846. The oligonucleotides are phosphodiester targeted  
CC against the translation initiation site (Q86650-55) or the 5'-cap  
CC region (Q86656-58) of human bcl-2 pre-mRNAs. A bcl-2 sense sequence  
CC (Q86649) was used as a control.  
SQ Sequence 20 BP; 4 A; 4 C; 10 G; 2 T;  
Query Match 100.0%; Score 18; DB 14; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.98e-02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 3 gaaggatgacgcacgtg 20  
|||||  
Cp 18 GAAGGATGGCGCAGCTG 1  
RESULT 2  
ID Q49817 standard; RNA; 22 BP.  
AC Q49817;  
DT Q3-MAY-1994 (first entry)  
DE Bcl-2 antisense oligonucleotide.  
KW Cell death; apoptosis; inhibition; de-inhibition; bcl-2 oncogene;  
KW expression; myc; ss.  
OS Synthetic.  
PN W09320200-A.  
PD 14-OCT-1993.  
PF 02-APR-1993; G00686.  
PR 02-APR-1992; GB-007275.  
PR 02-APR-1992; GB-007276.  
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.  
PI Evan GI;  
DR WPI; 93-336908/42.  
PT Treating tumour cells by de-inhibiting Myc-induced apoptosis -  
PT esp. by inhibiting expression of the BCL-2 oncogene e.g. with  
PT antisense oligo:nucleotide(s), also increasing survival of  
PT cultured cells by expressing BCL-2  
PS Disclosure; Page 58; 109pp; English.  
CC A DNA construct comprising the bcl-2 coding sequence under control  
CC of elements allowing its expression is claimed. Myc-induced cell  
CC death can be inhibited in cultured cells by expressing bcl-2.  
CC Myc-induced cell death can be de-inhibited in tumour cells by admin.  
CC of bcl-2 antisense oligonucleotides.  
SQ Sequence 22 BP; 2 A; 12 C; 4 G; 4 U;  
Query Match 100.0%; Score 16; DB 8; Length 22;  
Best Local Similarity 77.8%; Pred. No. 3.98e-02;  
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
Db 3 cagcgugcgccauccuuc 20  
|||||  
Qy 1 CAGCGTGGCCATCCTTC 18  
RESULT 3  
ID Q49816 standard; DNA; 22 BP.  
AC Q49816;

DT Q3-MAY-1994 (first entry)  
DE Bcl-2 antisense oligonucleotide.  
KW Cell death; apoptosis; inhibition; de-inhibition; bcl-2 oncogene;  
KW expression; myc; ss.  
OS Synthetic.  
PN W09320200-A.  
PD 14-OCT-1993.  
PF 02-APR-1993; G00686.  
PR 02-APR-1992; GB-007275.  
PR 02-APR-1992; GB-007276.  
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.  
PI Evan GI;  
DR WPI; 93-336908/42.  
PT Treating tumour cells by de-inhibiting Myc-induced apoptosis -  
PT esp. by inhibiting expression of the BCL-2 oncogene e.g. with  
PT antisense oligo:nucleotide(s), also increasing survival of  
PT cultured cells by expressing BCL-2  
PS Disclosure; Page 58; 109pp; English.  
CC A DNA construct comprising the bcl-2 coding sequence under control  
CC of elements allowing its expression is claimed. Myc-induced cell  
CC death can be inhibited in cultured cells by expressing bcl-2.  
CC Myc-induced cell death can be de-inhibited in tumour cells by admin.  
CC of bcl-2 antisense oligonucleotides.  
SQ Sequence 22 BP; 2 A; 12 C; 4 G; 4 T;  
Query Match 100.0%; Score 18; DB 8; Length 22;  
Best Local Similarity 100.0%; Pred. No. 3.98e-02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 3 cagcgtgcgcacatcttc 20  
|||||  
Qy 1 CAGCGTGGCCATCCTTC 18  
RESULT 4  
ID Q86644 standard; DNA; 35 BP.  
AC Q86644;  
DT 27-SEP-1995 (first entry)  
DE Bcl-2 translation initiation region.  
KW Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;  
KW leukemia; lymphoma; solid tumor; breast cancer; autoimmune disease;  
KW ss.  
OS Synthetic.  
PN W09308350-A.  
PD 30-MAR-1993.  
PF 20-SEP-1994; U10725.  
PR 20-SEP-1993; US-124256.  
PA (REED/) REED J C.  
PI Reed JC;  
DR WPI; 95-139394/18.  
PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment  
PT of human solid tumours, esp. breast cancer  
PS Disclosure; Page 13; 108pp; English.  
CC The antisense oligonucleotide T1-AS (Q86643) straddles the  
CC translation-initiation site in the mRNA coding strand of the human  
CC bcl-2 gene and is complementary to this region. It reduces the  
CC expression of bcl-2 gene product thereby inducing programmed cell  
CC death of certain cancer cells. The corresp. sense bcl-1 sequence  
CC was synthesized for use as a control.  
SQ Sequence 35 BP; 6 A; 8 C; 13 G; 8 T;

```
Query Match      100.0%; Score 18; DB 14; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.98e-02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 13 gaagatggcgacgctg 30
    |||||
Cp 18 GAAGATGGCGCAGCTG 1

RESULT 5
ID Q49815 standard; DNA; 765 BP.
AC Q49815;
DT C3-MAY-1994 (first entry)
DE Bcl-2.
KW Cell death; apoptosis; inhibition; de-inhibition; bcl-2 oncogene;
KW expression; myc; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 31..750
FT /*tag= a
FN W09320200-A.
PD 14-OCT-1993.
PF 02-APR-1993; G00686.
PR 02-APR-1992; GB-007275.
PR 02-APR-1992; GB-007276.
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
PI Evan G;
DR WPI; 93-336908/42.
DR P-PSDB; R42312.
PT Treating tumour cells by de-inhibiting Myc-induced apoptosis -
PT esp. by inhibiting expression of the Bcl-2 oncogene e.g. with
PT antisense oligo:nucleotide(s), also increasing survival of
PT cultured cells by expressing Bcl-2
PS Claim 26; Page 76-77; 109pp; English.
CC A DNA construct comprising the bcl-2 coding sequence under control
CC of elements allowing its expression is claimed. Myc-induced cell
CC death can be inhibited in cultured cells by expressing bcl-2.
CC Myc-induced cell death can be de-inhibited in tumour cells by admin.
CC of bcl-2 antisense oligonucleotides.
SQ Sequence 765 BP; 120 A; 251 C; 250 G; 144 T;

Query Match      100.0%; Score 18; DB 8; Length 765;
Best Local Similarity 100.0%; Pred. No. 3.98e-02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 26 gaagatggcgacgctg 43
    |||||
Cp 18 GAAGATGGCGCAGCTG 1

RESULT 6
ID N81293 standard; DNA; 831 BP.
AC N81293;
DT 17-DEC-1990 (first entry)
DE Sequence of bcl-2 cDNA corresp. to the 3.5 kb transcript encoding
DE Bcl-2-beta
KW B-cell neoplasm; diagnosis; follicular lymphomas; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
```

```
FT CDS 147..764
FT /*tag= a
FN EP-252685-A.
PD 13-JAN-1988.
PF 02-JUL-1987; 305863.
PR 09-JUL-1986; US-883687.
PA (WIST-) Wistar Corp.
PI Tsujimoto Y, Croce Ch;
DR WPI; 88-008633/02.
DR P-PSDB; P80988.
PT Detection of B-cell neoplasms -
PT by extn. of proteins or RNA from B-cells and quantitation using
PT specific antibody or DNA probe
PS Claim 8; Fig 3; 23pp; English.
CC Human bcl-2 gene substantially free of introns is claimed. Also claimed
CC is a substantially pure preparation of a protein having an N-terminal
CC encoded by the first exon of the human bcl-2 gene the protein being
CC bcl-2-alpha having about 239 (P80987) or 205 (P80988) residues. B-cell
CC neoplasms which are associated with t(14;18) chromosome translocations
CC cause an increase in expression of both the mRNA and the protein prods.
CC of the bcl-2 gene. This is used to detect B-cell neoplasms including
CC follicular lymphomas as well as other lymphomas. Bacterial isolates
CC available as ATCC 67147 and 67148 can be used to express gene prods.
CC alpha (n81292) and beta (n91293) resp. in bacteria.
SQ Sequence 831 BP; 138 A; 254 C; 290 G; 149 T;

Query Match      100.0%; Score 18; DB 1; Length 831;
Best Local Similarity 100.0%; Pred. No. 3.98e-02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 142 gaagatggcgacgctg 159
    |||||
Cp 18 GAAGATGGCGCAGCTG 1

RESULT 7
ID Q86661 standard; DNA; 5086 BP.
AC Q86661;
DT 27-SEP-1995 (first entry)
DE Human bcl-2 gene.
KW Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
KW chemoresistance; ss.
OS Homo sapiens.
PN W09508350-A.
PD 30-MAR-1995.
PR 20-SEP-1994; U10725.
PR 20-SEP-1993; US-124256.
PA (REED/) REED J C.
PI Reed JC;
DR WPI; 95-139394/18.
PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
PT of human solid tumours, esp. breast cancer
PS Disclosure; Page 65-68; 108pp; English.
CC Reversal of chemoresistance of tumor cells by antisense-mediated
CC reduction of bcl1-2 expression was demonstrated using the
CC oligonucleotide given in Q86659. This is antisense to the first
CC 6 codons of the bcl-2 ORF.
SQ Sequence 5086 BP; 1261 A; 1224 C; 1287 G; 1314 T;

Query Match      100.0%; Score 18; DB 14; Length 5086;
```

Best Local Similarity 100.0%; Pred. No. 3.98e-02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1454 gaagatggcgcacgtg 1471  
|||||  
Cp 18 GAAGGATGGCGCAGCTG 1

RESULT 8  
ID Q54631 standard; cDNA to mRNA; 5086 BP.  
AC Q54631;  
DT 23-JUN-1994 (first entry)  
DE Human oncogene bcl-2 coding sequence.  
KW Cell death; senescence; programmed cell death; ced-9; myocardial  
KW infarction; stroke; brain injury; neurodegenerative disease;  
KW muscular degenerative disease; ageing; hypoxia; ischaemia; toxemia;  
KW infection; hair loss; neoplasia; cancer; ced-3; ced-4; bcl-2;  
KW oncogene; aa.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 1459..2178  
FT /\*tag= a

FT /product= Bcl-2.  
PN M09325683-A.  
PD 23-DEC-1993.  
PF 14-JUN-1993; U05651.  
PR 12-JUN-1992; US-898933.  
PR 10-AUG-1992; US-927691.  
PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
PI Hengartner M, Horvitz HR;  
DR WPI; 94-007540/01.  
DR P-PSDB; R47344.  
PT Caenorhabditis elegans cell death-protective gene - used to  
develop agents for preventing cell death or for reducing  
population of cells

PS Disclosure; Page 61-64; 112pp; English.  
CC The protein product of the human oncogene bcl-2 was found to have a  
CC similar sequence to the ced-9 protein. ced-9 is essential for  
CC C. elegans development and apparently functions by protecting cells  
CC during development from programmed cell death. ced-9 was shown to  
CC function by antagonising the activities of cell death genes ced-3  
CC and ced-4. The ced-9 gene can be used for developing agents for  
CC treating a condition characterised by increased cell death such as  
CC myocardial infarction, stroke, traumatic brain injury,  
CC neurodegenerative disease, muscular degenerative disease, ageing,  
CC hypoxia, ischaemia, toxemia, infection or hair loss. It can also  
CC be used for reducing a population of cells in the treatment of  
CC neoplastic growth cancerous tissue, infected cells or autoreactive  
CC immune cells.  
SQ Sequence 5086 BP; 1262 A; 1222 C; 1288 G; 1314 T;

Query Match 100.0%; Score 18; DB 9; Length 5086;  
Best Local Similarity 100.0%; Pred. No. 3.98e-02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1454 gaagatggcgcacgtg 1471  
|||||  
Cp 18 GAAGGATGGCGCAGCTG 1

RESULT 9  
ID N81292 standard; cDNA; 5105 BP.  
AC N81292;  
DT 17-DEC-1990 (first entry)  
DE Sequence of bcl-2 cDNA corresp. to the 5.5 kb transcript encoding  
DE bcl-2-alpha  
KW B-cell neoplasm; diagnosis; follicular lymphomas; aa.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 1459..2178  
FT /\*tag= a

FT EP-252685-A.  
PN 13-JAN-1988.  
PF 02-JUL-1987; 305863.  
PR 09-JUL-1986; US-883687.  
PA (WIST-) Wistar Corp.  
PI Tsujimoto Y, Croce CM;  
DR WPI; 88-008633/02.  
DR P-PSDB; P80987.  
PT Detection of B-cell neoplasms -  
PT by extn. of proteins or RNA from B-cells and quantitation using  
PT specific antibody or DNA probe  
PS Claim 8; Fig 2A-2D; 23pp; English.  
CC A human bcl-2 gene substantially free of introns is claimed. Also claimed  
CC is a substantially pure preparation of a protein having an N-terminal end  
CC encoded by the first exon of the human bcl-2 gene wherein said protein is  
CC bcl-2-alpha having about 239 (P80987) or 205 (P80988) AA residues. B-cell  
CC neoplasms which are associated with t(14;18) chromosome translocations  
CC cause an increase in the expression of both mRNA and the protein prods.  
CC of the bcl-2 gene. This is used to detect B-cell neoplasms including  
CC follicular lymphomas as well as other lymphomas. Bacterial isolates  
CC available as ATCC 67147 and 67148 can be used to express gene prods.  
CC alpha (n81292) and beta (n91293) resp. in bacteria. 1313 T;  
SQ Sequence 5105 BP; 1281 A; 1225 C; 1286 G; 1313 T;

Query Match 100.0%; Score 18; DB 1; Length 5105;  
Best Local Similarity 100.0%; Pred. No. 3.98e-02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1454 gaagatggcgcacgtg 1471  
|||||  
Cp 18 GAAGGATGGCGCAGCTG 1

RESULT 10  
ID Q51746 standard; cDNA; 91 BP.  
AC Q51746;  
DT 31-MAY-1994 (first entry)  
DE Oligonucleotide probe MK14-A  
KW Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;  
KW aa.  
OS Synthetic.  
PN EP-571911-A.  
PD 01-DEC-1993.  
PF 24-MAY-1993; 108325.  
PR 26-MAY-1992; US-889651.  
PA (BECT ) BECTON DICKINSON CO.  
PI Shank DD, Spears PA;  
DR WPI; 93-378844/48.  
PT New oligo:nucleotide probes specific for Mycobacteria - used for

PT detection and amplification of Mycobacteria nucleic acid in  
 samples  
 PS Claim 3; Page 14; 23pp; English.  
 CC Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14  
 CC (Q51735). It hybridized to all spp. of mycobacteria tested, but  
 CC cross reacted to a few non-mycobacterial spp. The probe may  
 CC be useful as an initial screen for mycobacterial infection.  
 CC See also Q51735-45 and Q51747-59.  
 SQ Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;

Query Match 94.4%; Score 17; DB 9; Length 91;  
 Best Local Similarity 0.0%; Pred. No. 1.66e-01;  
 Matches 0; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

Db 38 svvvvhhvvvhhvhy 54

Cp 18 GAAGGATGGCGCAGCT 2

## RESULT 11

ID Q51746 standard; cDNA; 91 BP.

AC Q51746;

DT 31-MAY-1994 (first entry)

DE Oligonucleotide probe MK14-A

KW Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;

KW as.

OS Synthetic.

PN EP-571911-A.

PD 01-DEC-1993.

PF 24-MAY-1993; 108325.

PR 26-MAY-1992; US-889631.

PA (BECT ) BECTON DICKINSON CO.

PI Shank DP, Spears PA;

DR WPI; 93-378844/48.

PT New oligo:nucleotide probes specific for Mycobacteria - used for  
 PT detection and amplification of Mycobacteria nucleic acid in  
 PT samples

PS Claim 3; Page 14; 23pp; English.

CC Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14

CC (Q51735). It hybridized to all spp. of mycobacteria tested, but

CC cross reacted to a few non-mycobacterial spp. The probe may

CC be useful as an initial screen for mycobacterial infection.

CC See also Q51735-45 and Q51747-59.

SQ Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;

Query Match 88.9%; Score 16; DB 9; Length 91;

Best Local Similarity 0.0%; Pred. No. 6.76e-01;

Matches 0; Conservative 17; Mismatches 1; Indels 0; Gaps 0;

Db 38 svvvvhhvvvhhvhy 55

Qy 1 CAGCGTGGCGCATCTTC 18

## RESULT 12

ID Q22825 standard; DNA; 1429 BP.

AC Q22825;

DT 22-JUL-1992 (first entry)

DE Sequence encoding ovine interleukin IL-1beta.

KW Vaccine; antigen; therapeutic agent; immune response enhancer; -

KW modulator; ss.  
 OS Ovis ammon aries.  
 FH Key Location/Qualifiers  
 FT sig\_peptide 46..384  
 FT /\*tag= a  
 FT mat\_peptide 385..846  
 FT /\*tag= b  
 FT misc\_feature 1166..1178  
 FT /\*tag= c  
 FT /label= motif  
 FT misc\_feature 1194..1203  
 FT /\*tag= d  
 FT /label= motif  
 FT misc\_feature 1342..1346  
 FT /\*tag= e  
 FT /label= motif  
 FT misc\_feature 1356..1360  
 FT /\*tag= f  
 FT /label= motif  
 FT polyA\_signal 1400..1405  
 FT /\*tag= g  
 PN WO9203374-A.  
 PD 05-MAR-1992.

PF 13-AUG-1991; AU0358.

PR 13-AUG-1990; AU-001698.

PR 11-DEC-1990; AU-003859.

PR 15-FEB-1991; AU-004821.

PR 21-JUN-1991; AU-006840.

PA (UYME-) UNIV MELBOURNE.

PA (AWOO ) AUSTRALIAN WOOL CORP.

PI Brandon MR, Andrews AE, Nash AD, Neeseus EN;

DR WPI; 92-096916/12.

DR P-PSDB; R2122.

PT Nucleotide sequences coding for ruminant cytokine(s) or receptors  
 PT - used for producing polypeptide(s) for therapeutic and/or  
 PT adjuvant uses in animals

PS Disclosure; Fig 2A; 93pp; English.

CC The inventors claim a DNA sequence coding for a polypeptide  
 CC exhibiting ruminant cytokine or cytokine receptor activity; ovine  
 CC interleukine (IL)-1alpha activity; ovine IL-1alpha activity; ovine  
 CC IL-6 activity; ovine tumour necrosis factor (TNF) alpha activity;

CC ovine IL-2 receptor alpha activity; ovine interferon (IFN)-lambda

CC activity; or ovine IL-2 activity or homologous sequences, derivs. or

CC mutants, or fragments. The recombinant polypeptides are also

CC claimed.

SQ Sequence 1429 BP; 416 A; 363 C; 315 G; 335 T;

Query Match 77.8%; Score 14; DB 3; Length 1429;

Best Local Similarity 100.0%; Pred. No. 1.02e+01;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1284 gtgcgccatcttc 1297

Qy 5 GTGCGCCATCTTC 18

## RESULT 13

ID Q56983 standard; DNA; 1559 BP.

AC Q56983;

DT 12-AUG-1994 (first entry)



DE Improved Heat-stable carbamylase gene.  
KW Decarbamylase; thermal stability; decarbamylation; heat stable;  
KW N-carbamoyl-D-alpha-aminoacid; point mutation; random mutation;  
KW transformant; E.coli; transform; immobilisation; resin; vector; ds.  
OS Agrobacterium radiobacter.  
FH Key Location/Qualifiers  
FT CDS  
FT /\*tag= a  
FT /product= heat\_stable\_carbamylase  
FN W09403613-A.  
PD 17-FEB-1994.  
PF 05-AUG-1993; J01101.  
PR 10-AUG-1992; JP-212692.  
PR 21-DEC-1992; JP-340078.  
PA (KANF ) KANEAFUCHI KAGAKU KOGYO KK.  
PI Ikenaka Y, Nanba H, Takahashi S, Takano M, Yajima K;  
DR WPI; 94-065701/08.  
DR P-PSDB; R46259  
PT DNA coding for a decarbamylase with improved thermal stability -  
PT can be used for decarbamylation of  
PT N-carbamoyl-D-alpha-aminoacid(s)  
PS Claim 18; Page 98-100; 177pp; Japanese.  
CC Sequence (Q56963) shows a DNA encoding a thermal stable decarbamylase.  
CC The enzyme's thermo-stability has been improved by modifying the  
CC decarbamylase gene using 'point' and 'random' mutations. These are  
CC shown in sequences (Q56964-92). Sequences (Q56993-996) are also  
CC improved carbamylases contained within various different vectors for  
CC transformation.  
SQ Sequence 1559 BP; 321 A; 477 C; 465 G; 296 T;  
Query Match 77.8%; Score 14; DB 10; Length 1559;  
Best Local Similarity 93.8%; Pred. No. 1.02e+01;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 1301 agggggcgccagctg 1316  
|||||  
Cp 16 AGGATGCGCGACGCTG 1  
RESULT 14  
ID Q56981 standard; DNA; 1559 BP.  
AC Q56981;  
DE Improved Heat-stable carbamylase gene.  
KW Decarbamylase; thermal stability; decarbamylation; heat stable;  
KW N-carbamoyl-D-alpha-aminoacid; point mutation; random mutation;  
KW transformant; E.coli; transform; immobilisation; resin; vector; ds.  
OS Agrobacterium radiobacter.  
FH Key Location/Qualifiers  
FT CDS  
FT /\*tag= a  
FT /product= heat\_stable\_carbamylase  
FN W09403613-A.  
PD 17-FEB-1994.  
PF 05-AUG-1993; J01101.  
PR 10-AUG-1992; JP-212692.  
PR 21-DEC-1992; JP-340078.  
PA (KANF ) KANEAFUCHI KAGAKU KOGYO KK.  
PI Ikenaka Y, Nanba H, Takahashi S, Takano M, Yajima K;

PI Yamada Y;  
DR WPI; 94-065701/08.  
DR P-PSDB; R46257.  
PT DNA coding for a decarbamylase with improved thermal stability -  
PT can be used for decarbamylation of  
PT N-carbamoyl-D-alpha-aminoacid(s)  
PS Claim 18; Page 92-94; 177pp; Japanese.  
CC Sequence (Q56963) shows a DNA encoding a thermal stable decarbamylase.  
CC The enzyme's thermo-stability has been improved by modifying the  
CC decarbamylase gene using 'point' and 'random' mutations. These are  
CC shown in sequences (Q56964-92). Sequences (Q56993-996) are also  
CC improved carbamylases contained within various different vectors for  
CC transformation.  
SQ Sequence 1559 BP; 321 A; 477 C; 465 G; 296 T;  
Query Match 77.8%; Score 14; DB 10; Length 1559;  
Best Local Similarity 93.8%; Pred. No. 1.02e+01;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 1301 agggggcgccagctg 1316  
|||||  
Cp 16 AGGATGCGCGACGCTG 1  
RESULT 15  
ID Q56989 standard; DNA; 1559 BP.  
AC Q56989;  
DE Heat-stable carbamylase gene.  
KW Decarbamylase; thermal stability; decarbamylation; heat stable;  
KW N-carbamoyl-D-alpha-aminoacid; point mutation; random mutation;  
KW transformant; E.coli; transform; immobilisation; resin; vector; ds.  
OS Agrobacterium radiobacter.  
FH Key Location/Qualifiers  
FT CDS  
FT /\*tag= a  
FT /product= heat\_stable\_carbamylase  
FN W09403613-A.  
PD 17-FEB-1994.  
PF 05-AUG-1993; J01101.  
PR 10-AUG-1992; JP-212692.  
PR 21-DEC-1992; JP-340078.  
PA (KANF ) KANEAFUCHI KAGAKU KOGYO KK.  
PI Ikenaka Y, Nanba H, Takahashi S, Takano M, Yajima K;  
DR WPI; 94-065701/08.  
DR P-PSDB; R46265.  
PT DNA coding for a decarbamylase with improved thermal stability -  
PT can be used for decarbamylation of  
PT N-carbamoyl-D-alpha-aminoacid(s)  
PS Claim 18; Page 113-115; 177pp; Japanese.  
CC Sequence (Q56963) shows a DNA encoding a thermal stable decarbamylase.  
CC The enzyme's thermo-stability has been improved by modifying the  
CC decarbamylase gene using 'point' and 'random' mutations. These are  
CC shown in sequences (Q56964-92). Sequences (Q56993-996) are also  
CC improved carbamylases contained within various different vectors for  
CC transformation.  
SQ Sequence 1559 BP; 323 A; 476 C; 466 G; 294 T;  
Query Match 77.8%; Score 14; DB 10; Length 1559;

Best Local Similarity 93.8%; Pred. No. 1.02e+01;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1301 aggaggcgacgctg 1316

|||||

Cp 16 AGGATGGCGACGCTG 1

Search completed: Tue Jul 1 13:06:02 1997  
Job time : 33 secs.